

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

Claims 1-17. (Cancelled).

Claim 18. (Currently Amended) A method of obtaining isolated selected mRNA species or isolated selected cDNA species useful for diagnosing or identifying breast cancer in a human comprising the steps of:

- (a) isolating mRNA from cells from blood of more than one human who are known to have very early stage breast cancer (breast cancer sample), ~~wherein said cells have not contacted the area of said breast cancer and said blood is obtained from a part of said humans distant to the area of said breast cancer,~~ wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) isolating mRNA from corresponding cells from blood of more than one normal human (normal sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (c) separating mRNA species or cDNA species present within each of the resulting isolated mRNA or isolated cDNA of step (a) and step (b), wherein the resulting separated mRNA species are

optionally subject to reverse transcription to obtain separated cDNA species;

- (d) selecting 10 or more mRNA species or 10 or more cDNA species from the resulting separated mRNA species or resulting separated cDNA species obtained in step (c), respectively, which are present at a different level in the normal sample than in the breast cancer sample by identifying a signal corresponding to each mRNA species or cDNA species, wherein the resulting selected 10 or more mRNA species are optionally subjected to reverse transcription to obtain 10 or more selected cDNA species; and
- (e) isolating the resulting 10 or more selected mRNA species or resulting 10 or more selected cDNA species obtained in step (d) to obtain isolated selected mRNA species or isolated selected cDNA species, wherein the resulting isolated selected mRNA species are optionally subjected to reverse transcription to obtain isolated selected cDNA species.

Claim 19. (Currently Amended) A method of preparing a gene transcript pattern probe kit comprising the steps of:

- (a) isolating mRNA from cells from blood of more than one human who are known to have very early stage breast cancer (breast cancer sample), ~~wherein said cells have not contacted the area of said breast cancer and said blood is obtained from a~~

~~part of said humans distant to the area of said breast cancer,~~ wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;

- (b) isolating mRNA from corresponding cells from blood of more than one normal human (normal sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (c) separating mRNA species or cDNA species present within each of the resulting isolated mRNA or isolated cDNA of step (a) and step (b), wherein the resulting separated mRNA species are optionally subject to reverse transcription to obtain separated cDNA species;
- (d) selecting 10 or more mRNA species or 10 or more cDNA species from the resulting separated mRNA species or resulting separated cDNA species obtained in step (c) respectively, which are present at a different level in the normal sample than in the breast cancer sample by identifying a signal corresponding to each mRNA species or cDNA species, wherein the resulting selected 10 or more mRNA species are optionally subjected to reverse transcription to obtain 10 or more selected cDNA species;
- (e) isolating the resulting 10 or more selected mRNA species or resulting 10 or more selected cDNA

species obtained in step (d) to obtain isolated selected mRNA species or isolated selected cDNA species, wherein the resulting isolated selected mRNA species are optionally subjected to reverse transcription to obtain isolated selected cDNA species; and

- (f) preparing at least one solid support carrying the resulting isolated selected mRNA species or isolated selected cDNA species of step (e) so as to form a gene transcript pattern probe kit.

Claim 20. (Previously Presented) The method as claimed in claim 18 or 19, wherein said separation in step (c) is performed by a non-sequence based separation technique.

Claim 21. (Previously Presented) The method as claimed in claim 18 or 19, wherein in steps (a) and (b), the resulting isolated mRNA is subjected to reverse transcription to obtain isolated cDNA.

Claim 22. (Previously Presented) The method as claimed in claim 21, wherein said isolated cDNA is amplified.

Claim 23. (Previously Presented) The method as claimed in claim 18 or 19, wherein in step (e), between 50 and 100 mRNA species or cDNA species are isolated and selected.

Claim 24. (Previously Presented) The method as claimed in claim 18 or 19, wherein, in step (e) between 10 and 500 mRNA species or cDNA species are isolated and selected.

Claim 25. (Previously Presented) The method as claimed in claim 18 or 19, wherein, in step (c), said separation technique is gel electrophoresis.

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Claim 26. (Previously Presented) The method as claimed in claim 19, wherein, prior to immobilizing in step (f), the resulting isolated selected mRNA species or isolated selected cDNA species of step (e) are amplified.

Claim 27. (Currently Amended) A method of preparing a standard gene transcript pattern characteristic of breast cancer of a human comprising the steps of:

- (a) isolating mRNA from cells from blood of more than one human who are known to have said breast cancer (breast cancer sample), ~~wherein said blood is obtained from a part of said humans distant to the area of said breast cancer,~~ wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to 10 or more mRNA species which are present at a different level in cells in a blood sample from more than one normal human than in corresponding cells in a blood sample from more than one human who are known to have said very early stage breast cancer, or to 10 or more cDNA species transcribed from said mRNA species, wherein the 10 or more mRNA species or cDNA species are specific for said breast cancer ~~and wherein said cells have not contacted the area of said breast cancer and said blood is obtained from a part of said humans distant to the~~

- ~~area of said breast cancer~~, wherein said mRNA or cDNA species are carried on a solid support; and
- (c) assessing the amount of hybridization so as to obtain said standard gene transcript pattern.

Claim 28. (Currently Amended) A method of preparing a test gene transcript pattern for breast cancer in a human comprising the steps of:

- (a) isolating mRNA from cells from blood of a test human suspected to have breast cancer, ~~wherein said blood is obtained from a part of said human distant to the suspected area of said breast cancer~~, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to 10 or more mRNA species which are present at a different level in cells in a blood sample from more than one normal human than in corresponding cells in a blood sample from more than one human who are known to have said very early stage breast cancer, or to 10 or more cDNA species transcribed from said mRNA species, wherein the 10 or more mRNA species or cDNA species are specific for said breast cancer ~~and wherein said cells have not contacted the area of said breast cancer and said blood is obtained from a part of said humans distant to the area of said breast cancer~~, wherein said mRNA

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or cDNA species are carried on a solid support;
and

- (c) assessing the amount of hybridization so as to obtain said test gene transcript pattern.

Claim 29. (Currently Amended) A method of diagnosing or identifying breast cancer in a test human comprising the steps of:

- (a) isolating mRNA from cells from blood of a test human, ~~wherein said blood is obtained from a part of said human distant to the area of said breast cancer,~~ wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to 10 or more mRNA species which are present at a different level in cells in a blood sample from more than one normal human than in corresponding cells in a blood sample from more than one human who are known to have said very early stage breast cancer, or to 10 or more cDNA species transcribed from said mRNA species, wherein the 10 or more mRNA species or cDNA species are specific for said breast cancer ~~and wherein said cells have not contacted the area of said breast cancer and said blood is obtained from a part of said humans distant to the area of said breast cancer,~~ wherein said mRNA or cDNA species are carried on a solid support;

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- (c) assessing the amount of hybridization so as to obtain a hybridization pattern; and
- (d) comparing the resulting hybridization pattern obtained in step (c) with a hybridization pattern obtained by hybridizing isolated mRNA or isolated cDNA prepared from corresponding cells from blood of more than one human who are known to have said breast cancer to the 10 or more mRNA species or 10 or more cDNA species transcribed from said mRNA species, wherein said mRNA species or cDNA species are carried on a solid support, so as to determine the degree of correlation indicative of the presence of said breast cancer, and so as to diagnose or identify said breast cancer in said test human.

Claim 30. (Previously Presented) The method as claimed in claim 27, 28 or 29, wherein in step (a), the resulting isolated mRNA is subjected to reverse transcription to obtain isolated cDNA.

Claim 31. (Previously Presented) The method as claimed in claim 30, wherein said isolated cDNA is amplified.

Claim 32. (Previously Presented) The method as claimed in claim 18, 19, 27, 28 or 29, wherein said isolated cDNA is labeled.

Claim 33. (Previously Presented) The method as claimed in claim 27, 28 or 29, wherein, in step (b), between 50 and 100 mRNA species or cDNA species are used.

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Claim 34. (Previously Presented) The method as claimed in claim 27, 28 or 29, wherein, in step (b), between 10 and 500 mRNA species or cDNA species are used.

Claim 35. (Previously Presented) The method as claimed in claim 19, 27, 28 or 29, wherein said solid support is a filter.

Claims 36-38. (Cancelled).